

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

O. FAMODU ET AL.

APPLICATION NO.: 09/831,088

INTERNATIONAL FILING DATE: 09 NOV 99 EXAMINER: INDIA L. EVANS

FOR: PLANT AMINOACYL-tRNA SYNTHETASES



CASE NO.: BB1270

GROUP ART UNIT: UNKNOWN

STATEMENT UNDER 37 CFR 1.821(g) and 1.825(b)Assistant Commissioner for Patents
Washington, DC 20231

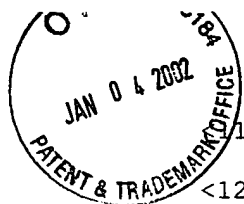
Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

The copy of the substitute Sequence Listing in computer readable form filed concurrently herewith is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith.

Respectfully submitted,

Thomas M. Rizzo, Ph.D.
Attorney For Applicants
Registration No. 41,272
Telephone: 302-892-7760
Facsimile: 302-892-1026Dated: November 15, 2001



SEQUENCE LISTING

<10> E. I. du Pont de Nemours and Company

<120> Plant Aminoacyl-tRNA Synthetases

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<140> US/09/831,683

<141> 2001-05-10

<150> 60/107,789

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tgataaagca	gggtaaagca	tataattgat	acacaccaaa	ggagcaaatg	aggaaagaga	1140
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<210> 10
 <211> 715
 <212> PRT
 <213> Zea mays

<400> 10
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 20 25 30

 Leu Ala Ala Gly Ser Ala Pro Thr Leu Gln Phe Ala Ser Gly Glu Ser
 35 40 45

 Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser
 50 55 60

 Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val
 65 70 75 80

 Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu
 85 90 95

 Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu
 100 105 110

 Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu
 115 120 125

 Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr
 130 135 140

 Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu
 145 150 155 160

 Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly
 165 170 175

 Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp
 180 185 190

 Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val
 195 200 205

 Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His
 210 215 220

 Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly
 225 230 235 240

 Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn
 245 250 255

Glu	Phe	Val	Glu	Asn	Leu	Leu	Lys	Asp	Ile	Glu	Thr	Leu	Gly	Ile	Lys	
			260					265					270			
Tyr	Asp	Ala	Val	Thr	Tyr	Thr	Ser	Asp	Tyr	Phe	Pro	Lys	Leu	Met	Glu	
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Pro	Lys	Glu	Gln	Met	Arg	Lys	Glu	Arg	Met	Asp	Gly	Ile	Glu	Ser	Arg	
305					310					315					320	
Cys	Arg	Asn	Asn	Thr	Val	Glu	Glu	Asn	Leu	Ser	Leu	Trp	Lys	Glu	Met	
				325					330					335		
Val	Asn	Gly	Thr	Glu	Arg	Gly	Met	Gln	Cys	Cys	Val	Arg	Gly	Lys	Leu	
			340					345					350			
Asp	Met	Gln	Asp	Pro	Asn	Lys	Ser	Leu	Arg	Asp	Pro	Val	Tyr	Tyr	Arg	
		355					360					365				
Cys	Asn	Thr	Asp	Pro	His	His	Arg	Val	Gly	Ser	Lys	Tyr	Lys	Val	Tyr	
	370					375					380					
Pro	Thr	Tyr	Asp	Phe	Ala	Cys	Pro	Phe	Val	Asp	Ala	Leu	Glu	Gly	Val	
385					390					395					400	
Thr	His	Ala	Leu	Arg	Ser	Ser	Glu	Tyr	His	Asp	Arg	Asn	Ala	Gln	Tyr	
				405					410					415		
Tyr	Arg	Ile	Leu	Gln	Asp	Met	Gly	Leu	Arg	Arg	Val	Glu	Ile	Tyr	Glu	
			420					425					430			
Phe	Ser	Arg	Leu	Asn	Met	Val	Tyr	Thr	Leu	Leu	Ser	Lys	Arg	Lys	Leu	
		435					440					445				
Leu	Trp	Phe	Val	Gln	Asn	Lys	Lys	Val	Glu	Asp	Trp	Thr	Asp	Pro	Arg	
	450					455					460					
Phe	Pro	Thr	Val	Gln	Gly	Ile	Val	Arg	Arg	Gly	Leu	Lys	Val	Glu	Ala	
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Leu	Ile	Gln	Phe	Ile	Leu	Gln	Gln	Gly	Ala	Ser	Lys	Asn	Leu	Asn	Leu	
				485					490					495		
Met	Glu	Trp	Asp	Lys	Leu	Trp	Thr	Ile	Asn	Lys	Lys	Ile	Ile	Asp	Pro	
			500					505					510			
Val	Cys	Ala	Arg	His	Thr	Ala	Val	Leu	Lys	Asp	Gln	Arg	Val	Ile	Phe	
		515					520					525				
Thr	Leu	Thr	Asn	Gly	Pro	Glu	Glu	Pro	Phe	Val	Arg	Ile	Leu	Pro	Arg	
	530					535					540					
His	Lys	Lys	Phe	Glu	Gly	Ala	Gly	Lys	Lys	Ala	Thr	Thr	Phe	Ala	Asn	
545					550					555					560	
Arg	Ile	Trp	Leu	Asp	Tyr	Ala	Asp	Ala	Ala	Ala	Ile	Asn	Lys	Gly	Glu	
				565				570						575		

Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys
 580 585 590
 Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu
 595 600 605
 Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile
 610 615 620
 Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser
 625 630 635 640
 Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro
 645 650 655
 Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn
 660 665 670
 Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg
 675 680 685
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 690 695 700
 Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser
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<210> 11
 <211> 1920
 <212> DNA
 <213> *Oryza sativa*

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 <223> n = A, C, G or T

<220>
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 <222> (238)
 <223> n = A, C, G or T

<220>
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 <223> n = A, C, G or T

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 tcgtggtgag gtcagttgga acttagacac gcttggtgat ttcgtgatta tgagaagcaa 720

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<210> 12
 <211> 555
 <212> PRT
 <213> *Oryza sativa*

<220>
 <221> UNSURE
 <222> (130)
 <223> Xaa = ANY AMINO ACID

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 His Leu Arg Arg Pro Ser Pro Ser Ala Pro Pro Pro Pro Arg Arg
 20 25 30
 His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala
 35 40 45
 Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr
 50 55 60
 Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp
 65 70 75 80
 Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser
 85 90 95
 Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly
 100 105 110
 Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys
 115 120 125
 Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe
 130 135 140
 Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys

145					150					155					160
Asn	Leu	Pro	Pro	Val	Tyr	Ile	Gly	Lys	Trp	Gly	Thr	Ala	Ser	Asp	Ala
				165					170					175	
Glu	Ile	Gln	Gln	Glu	Leu	Glu	Lys	Gly	Thr	Pro	Tyr	Thr	Tyr	Arg	Phe
			180					185					190		
Arg	Val	Pro	Lys	Glu	Gly	Ser	Leu	Lys	Ile	Asn	Asp	Leu	Ile	Arg	Gly
		195					200					205			
Glu	Val	Ser	Trp	Asn	Leu	Asp	Thr	Leu	Gly	Asp	Phe	Val	Ile	Met	Arg
	210					215					220				
Ser	Asn	Gly	Gln	Pro	Val	Tyr	Asn	Phe	Cys	Val	Thr	Val	Asp	Asp	Ala
225					230					235					240
Thr	Met	Arg	Ile	Ser	His	Val	Ile	Arg	Ala	Glu	Glu	His	Leu	Pro	Asn
				245					250					255	
Thr	Leu	Arg	Gln	Ala	Leu	Ile	Tyr	Lys	Ala	Leu	Gly	Phe	Pro	Met	Pro
			260					265					270		
Ser	Phe	Ala	His	Val	Ser	Leu	Ile	Leu	Ala	Pro	Asp	Arg	Ser	Lys	Leu
	275						280					285			
Ser	Lys	Arg	His	Gly	Ala	Thr	Ser	Val	Gly	Gln	Tyr	Lys	Glu	Met	Gly
	290					295					300				
Tyr	Leu	Pro	Gln	Ala	Met	Val	Asn	Tyr	Leu	Ala	Leu	Leu	Gly	Trp	Gly
305					310					315					320
Asp	Gly	Thr	Glu	Asn	Glu	Phe	Phe	Thr	Ile	Asp	Asp	Leu	Val	Glu	Lys
				325					330					335	
Phe	Thr	Ile	Asn	Arg	Val	Asn	Lys	Ser	Gly	Ala	Val	Phe	Asp	Ala	Val
			340					345					350		
Lys	Leu	Lys	Trp	Met	Asn	Gly	Gln	His	Leu	Arg	Ser	Phe	Pro	Pro	Asp
	355						360					365			
Val	Leu	Ile	Lys	Ser	Phe	Glu	Asp	Arg	Trp	Lys	Asp	Thr	Gly	Ile	Leu
	370					375					380				
Gln	Glu	Ser	Glu	Ser	Gly	Phe	Ala	Lys	Glu	Ala	Ala	Glu	Leu	Leu	Lys
385					390					395					400
Asp	Gly	Ile	Asp	Leu	Ile	Thr	Asp	Ala	Asp	Ala	Ala	Leu	Ser	Asn	Leu
				405					410					415	
Leu	Ser	Tyr	Pro	Leu	His	Ala	Thr	Leu	Ser	Ser	Asp	Glu	Ala	Lys	Ser
			420					425					430		
Val	Val	Gln	Asp	Lys	Leu	Ser	Glu	Val	Ala	Ser	Gly	Leu	Ile	Ser	Ala
	435						440					445			
Tyr	Asp	Ser	Gly	Glu	Leu	Cys	Gln	Ala	Leu	Ala	Glu	Gly	Arg	Asp	Gly
	450					455					460				
Trp	Gln	Lys	Trp	Val	Lys	Ile	Phe	Gly	Lys	Ser	Leu	Lys	Arg	Lys	Gly

465

470

475

480

Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly Lys Leu His
 485 490 495

Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr
 500 505 510

Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg
 515 520 525

Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln
 530 535 540

Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser
 545 550 555

<210> 13

<211> 731

<212> DNA

<213> Glycine max

<400> 13

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 tttctcaagt ctctgctctc tccgaacaac caccaccgt tcgcttctg ttcgctcctt 180
 ctcccaccgg aaacctccac gtcggcggtg cccgaacggc cctcttcaac tacttggttcg 240
 caaggtccaa aggtgggaaa ttgtgtctga gaattgagga cactgacttg gagaggtcca 300
 caagggagtc tgaggaggcc atgctcaaag atctttcttg gcttggactt gattgggatg 360
 aagggcctgg tgttggaggg gattatggtc cttataggca gtctgatagg aattctttat 420
 acaagcaatt tgcggataac ctacaccaat ccggtcatgt ttatcgctgc ttctgttcta 480
 atgaggaact agagaaaatg aaggaggatg ctaaactaaa gcaactgcct ccagtgtaca 540
 caggtaaatg ggccagtgc acaaatgagg aagtagaaga agagctagca aaaggaactc 600
 cttacactta ccggttccga gtccctaaag gaagtttaaa aattaatgat caaatacgag 660
 gcgaagttag ttggaacttg gatacgcttg gagattttgt gataatgagg agtaatggtc 720
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<210> 14

<211> 404

<212> PRT

<213> Glycine max

<400> 14

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 20 25 30

Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr
 35 40 45

Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
 50 55 60

Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg
 65 70 75 80

Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His
 85 90 95

Gln	Ser	Gly	His	Val	Tyr	Arg	Cys	Phe	Cys	Ser	Asn	Glu	Glu	Leu	Glu	100	105	110
Lys	Met	Lys	Glu	Asp	Ala	Lys	Leu	Lys	Gln	Leu	Pro	Pro	Val	Tyr	Thr	115	120	125
Gly	Lys	Trp	Ala	Ser	Ala	Thr	Asn	Glu	Glu	Val	Glu	Glu	Glu	Leu	Ala	130	135	140
Lys	Gly	Thr	Pro	Tyr	Thr	Tyr	Arg	Phe	Arg	Val	Pro	Lys	Gly	Ser	Leu	145	150	155
Lys	Ile	Asn	Asp	Gln	Ile	Arg	Gly	Glu	Val	Ser	Trp	Asn	Leu	Asp	Thr	165	170	175
Leu	Gly	Asp	Phe	Val	Ile	Met	Arg	Ser	Asn	Gly	Gln	Pro	Val	Tyr	Asn	180	185	190
Phe	Cys	Val	Thr	Val	Asp	Asp	Ala	Thr	Met	Ala	Ile	Ser	His	Val	Ile	195	200	205
Arg	Ala	Glu	Glu	His	Leu	Pro	Asn	Thr	Leu	Arg	Gln	Ala	Leu	Ile	Tyr	210	215	220
Lys	Ala	Leu	Gly	Phe	Pro	Met	Pro	His	Phe	Ala	His	Val	Ser	Leu	Ile	225	230	235
Leu	Ala	Pro	Asp	Arg	Ser	Lys	Leu	Ser	Lys	Arg	His	Gly	Ala	Thr	Ser	245	250	255
Val	Gly	Gln	Phe	Arg	Asp	Met	Gly	Tyr	Leu	Pro	Gln	Ala	Met	Val	Asn	260	265	270
Tyr	Leu	Ala	Leu	Leu	Gly	Trp	Gly	Asp	Gly	Thr	Glu	Asn	Glu	Phe	Phe	275	280	285
Thr	Leu	Glu	Gln	Leu	Val	Glu	Lys	Phe	Thr	Ile	Glu	Arg	Val	Asn	Lys	290	295	300
Ser	Gly	Ala	Ile	Phe	Asp	Ser	Thr	Lys	Leu	Arg	Trp	Met	Asn	Gly	Gln	305	310	315
His	Leu	Arg	Ser	Leu	Pro	Ser	Glu	Glu	Leu	Asn	Arg	Ile	Ile	Gly	Glu	325	330	335
Arg	Trp	Lys	Asp	Ala	Gly	Ile	Ala	Thr	Glu	Ser	Gln	Gly	Ile	Phe	Ile	340	345	350
Gln	Asp	Ala	Val	Leu	Leu	Leu	Lys	Asp	Gly	Ile	Asp	Leu	Ile	Thr	Asp	355	360	365
Ser	Glu	Lys	Ala	Leu	Ser	Ser	Leu	Leu	Ser	Tyr	Pro	Leu	Tyr	Glu	Thr	370	375	380
Leu	Ala	Ser	Ala	Glu	Gly	Lys	Pro	Ile	Leu	Glu	Asp	Gly	Val	Ser	Glu	385	390	395
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<211> 407
<212> DNA
<213> Triticum aestivum

<220>
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<223> n = A, C, G or T

<220>
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<222> (250)
<223> n = A, C, G or T

<220>
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<222> (293)
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<220>
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<222> (401)
<223> n = A, C, G or T

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gcaaggacgc gattcgcgcc gtcaccaaca gggaatcttc atcttggttc cctacgtacg 180
gccctcttca attacctgat tgcaaaagct acacgcggta aattcatcct acgcatagag 240
gacacagatn agtcaaggac tgttcctggt gcgattgaaa aactctgcgc tgntttgaga 300
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<210> 16
<211> 79
<212> PRT
<213> Triticum aestivum

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 <222> (55)
 <223> Xaa = ANY AMINO ACID

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 <222> (69)
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 20 25 30
 Leu Phe Asn Tyr Leu Ile Ala Lys Ala Thr Arg Gly Lys Phe Ile Leu
 35 40 45
 Arg Ile Glu Asp Thr Asp Xaa Ser Arg Thr Val Pro Gly Ala Ile Glu
 50 55 60
 Lys Leu Cys Ala Xaa Leu Arg Trp Gly Gly Leu Lys Arg Asp Lys
 65 70 75

<210> 17
 <211> 2387
 <212> DNA
 <213> Zea mays

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tcaggttggc tccatagcgg ctggtggtcg gtacgacaac cttgtgggta tgttttagtgg 1740
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 <212> PRT
 <213> Zea mays

<400> 18

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 20 25 30

Asp Pro Lys Cys Pro Gly Leu Glu Ser Leu Val Glu Lys Val Lys Glu
 35 40 45

Ile Val Glu Ser Asn Glu Val Arg Arg Leu Pro Lys Ile Pro Lys Gly
 50 55 60

Thr Arg Asp Phe Gly Lys Glu Gln Met Ala Ile Arg Glu Arg Ala Phe
 65 70 75 80

Ser Ile Ile Thr Ser Val Phe Lys Met His Gly Ala Thr Ala Leu Asp
 85 90 95

Thr Pro Val Phe Glu Leu Arg Glu Thr Leu Met Gly Lys Tyr Gly Glu
 100 105 110

Asp Ser Lys Leu Ile Tyr Asp Leu Ala Asp Gln Gly Gly Glu Leu Cys
 115 120 125

Ser Leu Arg Tyr Asp Leu Thr Val Pro Phe Ala Arg Tyr Val Ala Met
 130 135 140

Asn Ser Ile Ser Ala Leu Lys Arg Tyr Gln Ile Ala Lys Val Tyr Arg
 145 150 155 160

Arg Asp Asn Pro Ser Lys Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp
 165 170 175

Phe Asp Ile Ala Gly Val Tyr Glu Pro Met Glu Pro Asp Phe Glu Val
 180 185 190

Ile Lys Val Leu Thr Glu Leu Leu Asn Gln Leu Asp Ile Gly Thr Tyr
 195 200 205

Glu Ile Lys Leu Asn His Arg Lys Leu Leu Asp Gly Met Leu Glu Ile
 210 215 220

Cys	Gly	Val	Pro	Pro	Gln	Lys	Phe	Arg	Thr	Val	Cys	Ser	Ser	Ile	Asp	225	230	235	240
Lys	Leu	Asp	Lys	Gln	Thr	Phe	Glu	Gln	Val	Lys	Lys	Glu	Leu	Val	Asp	245	250	255	
Glu	Lys	Gly	Ile	Ser	Asn	Glu	Thr	Ala	Asp	Glu	Ile	Gly	Asn	Leu	Val	260	265	270	
Lys	Thr	Arg	Gly	Pro	Pro	Leu	Glu	Val	Leu	Met	Glu	Leu	Arg	Lys	Glu	275	280	285	
Gly	Ser	Lys	Phe	Met	Asn	Asn	Val	Gly	Ser	Val	Ala	Ala	Leu	Asn	Glu	290	295	300	
Leu	Glu	Ile	Leu	Phe	Lys	Ala	Leu	Asp	Lys	Ala	Asn	Ala	Ile	Ser	Lys	305	310	315	320
Ile	Thr	Phe	Asp	Leu	Ser	Leu	Ala	Arg	Gly	Leu	Asp	Tyr	Tyr	Thr	Gly	325	330	335	
Val	Ile	Tyr	Glu	Ala	Val	Phe	Lys	Gly	Ala	Ala	Gln	Val	Gly	Ser	Ile	340	345	350	
Ala	Ala	Gly	Gly	Arg	Tyr	Asp	Asn	Leu	Val	Gly	Met	Phe	Ser	Gly	Lys	355	360	365	
Gln	Ile	Pro	Ala	Val	Gly	Val	Ser	Leu	Gly	Ile	Glu	Arg	Val	Phe	Ala	370	375	380	
Ile	Met	Glu	Gln	Gln	Glu	Lys	Glu	Arg	Asn	Glu	Lys	Ile	Arg	Pro	Thr	385	390	395	400
Glu	Thr	Glu	Val	Leu	Val	Ser	Ile	Leu	Gly	Lys	Asp	Leu	Thr	Leu	Ala	405	410	415	
Ala	Glu	Leu	Val	Ser	Glu	Leu	Trp	Asn	Ala	Gly	Ile	Lys	Ala	Glu	Phe	420	425	430	
Lys	Leu	Thr	Thr	Arg	Val	Ala	Asn	His	Ile	Lys	Tyr	Ala	Leu	Gln	Ser	435	440	445	
Ser	Ile	Pro	Trp	Met	Val	Leu	Val	Gly	Glu	Ser	Glu	Leu	Gln	Lys	Gly	450	455	460	
Thr	Val	Lys	Leu	Lys	Asp	Val	Glu	Ala	Asn	Gln	Glu	Glu	Glu	Val	Asp	465	470	475	480
Arg	Lys	Asp	Phe	Val	Arg	Glu	Leu	Lys	Lys	Arg	Leu	Ser	Lys	Ser		485	490	495	

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gtcgaaaggt	tctgcaagaa	gtattaaatt	gttattcagt	accagaaaat	ttattttggca	180
aggtctgcgt	cattattgat	aaaattgaga	aaattccagc	tgacgagata	aagaaagagt	240
tgaaagctgt	tggtctatct	caagaggctg	tccaggagct	attgcaagtc	ctttctgtga	300
agtcattgac	cgagttagaa	gagagacttg	ggagcagtg	ggaagcagtt	gctgatctga	360
aacagctatt	ctcccttgct	gaaaaaattg	gttactctaa	atggcttcaa	tttgatgcat	420
cagtgtgtcg	aggtcttgct	tactacactg	gcattgtatt	tgagggtttt	gaccgagaag	480
gaaagctgcg	agctatctgt	ggtggtggtc	gatatgatca	tttgttctca	acttttggtg	540
ctgatgacat	tgctgcatgt	ggttttggtg	ttggtgatgc	aagtcatagt	ggaattgctc	600
aaaagagaan	ggtctgttac	cgggaagctt	aacttgcaaa	tagatgacat	tgtgtgtgcc	660
ttggaccaaa	gatcttcaag	ggatgtgctg	ctatgggccc	caacaatctc	agngaaaaan	720
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<211> 243

<212> PRT

<213> Glycine max

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      20           25           30

Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
      35           40           45

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
      50           55           60

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
      65           70           75           80

Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val
      85           90           95

Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser
      100          105          110

Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys
      115          120          125

Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly
      130          135          140

Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly
      145          150          155          160

Lys Leu Arg Ala Ile Cys Gly Gly Gly Arg Tyr Asp His Leu Phe Ser
      165          170          175

Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp
      180          185          190

Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu
      195          200          205

Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys
      210          215          220

Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile
      225          230          235          240

Val Glu Val
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<210> 21

<211> 1164

<212> DNA

<213> Triticum aestivum

<400> 21

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tgacaagctg gggaaactga gtagggaaga aattgagaag gaattgattt caactgggct 180
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tgatactac	acagggattg	tttttgaggc	ttttgatagg	gaaggggaac	tgagagcgat	420
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ctgtggcttt	ggatttggag	atgctgtcat	agtggagctg	ctgaaagaaa	agggtctttt	540
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gccagcatct	agtgttgcac	cctgtctgcg	gaagaagggc	agatctgtag	accttgtaga	660
agacaagcgt	ctgaaatggg	tgttcaaaca	tgctgagagg	ataaacgcta	gcaggctgat	720
cttggttggg	aaatccgagt	gggagcgagg	catggtccgt	gtgaagatac	tatcaaccag	780
agaagagttc	gaggtcaagg	cgggcgaatt	gcagtagctg	ttagctgata	tggtcgattt	840
gaaggtttga	cttgtccctt	ttcttctttc	tgatcatctt	caacactgta	agttttgcaa	900
ttcacgtcgt	gtatacaaac	aattaggtgg	ctttgaatgc	tattgccatc	ttctttcgga	960
tcattcacct	tgcaacaaac	aaagaaattg	taggttttgc	cattcaccaa	catgtattga	1020
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1140
aaaaaaaaaa	aaaaaaaaaa	aaaa				1164

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 <212> PRT
 <213> Triticum aestivum

<400> 22

Lys	Leu	Gly	Ile	Thr	Ser	Ser	Asp	Val	Gly	Ile	Arg	Leu	Ser	Ser	Arg
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Lys	Val	Leu	Gln	Ala	Val	Leu	Asp	Met	Tyr	Ser	Val	Pro	Gln	His	Leu
			20					25					30		
Phe	Thr	Gln	Val	Cys	Val	Ile	Val	Asp	Lys	Leu	Gly	Lys	Leu	Ser	Arg
		35					40					45			
Glu	Glu	Ile	Glu	Lys	Glu	Leu	Ile	Ser	Thr	Gly	Leu	Ser	Ser	Glu	Ala
	50					55					60				
Val	Gln	Gly	Ile	Ile	Glu	Val	Leu	Ser	Leu	Lys	Ser	Leu	Ser	Lys	Leu
65					70					75					80
Glu	Glu	Val	Leu	Gly	Ser	Gly	Val	Glu	Ala	Val	Ala	Asp	Leu	Lys	Lys
				85					90					95	
Leu	Phe	Ser	Leu	Ala	Glu	Gln	Tyr	Gly	Tyr	Ser	Asp	Trp	Ile	Cys	Phe
			100					105					110		
Asp	Ala	Ser	Val	Val	Arg	Gly	Leu	Ala	Tyr	Tyr	Thr	Gly	Ile	Val	Phe
			115				120					125			
Glu	Ala	Phe	Asp	Arg	Glu	Gly	Glu	Leu	Arg	Ala	Ile	Cys	Gly	Gly	Gly
	130					135					140				
Arg	Tyr	Asp	Arg	Leu	Leu	Ser	Thr	Phe	Gly	Thr	Glu	Asp	Val	Pro	Ala
145				150					155					160	
Cys	Gly	Phe	Gly	Phe	Gly	Asp	Ala	Val	Ile	Val	Glu	Leu	Leu	Lys	Glu
				165					170					175	
Lys	Gly	Leu	Leu	Pro	Asp	Leu	Pro	Arg	Gln	Ile	Asp	Asp	Ile	Val	Phe
			180					185					190		

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys
195 200 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu
210 215 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile
225 230 235 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile
245 250 255

Leu Ser Thr Arg Glu Glu Phe Glu Val Lys Ala Gly Glu Leu Gln
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 ttaagagtga tgggtggcttc aactatgcct caacagactt aactgctctt tggatcggc 180
 tcaatgttga gcaggcagag tggatcatat atgttacaga tgttggtcag cagcagcact 240
 ttgacatggg ttccagtgcg gcaaagatgg ccggttggct cccagatcca agtgaagaaga 300
 agtttccgaa aacaagccat gttggatttg gtcttgttct tggttcaaga tggcaagcgg 360
 ttccgaaccc gcagtactga ggttggttca ttggttagagc tacttgatga ggctaaatct 420
 cggagcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480
 gatgangaat tagagcaaac ttcagaggct gttggatatg gtgctgtgaa gtacgctgat 540
 ctaaaaaata acaggctcac taattacaca tttagttttg aacaaatgct gagcgataag 600
 ggaaatactg ctgtgtacct tcagtatgca catgctcgta tttgttccat tattcggaaa 660
 tccaacaaga acgtggnaga ctgaagagat ggagccattt ctctcgacca tccggattag 720
 cgctgttggg gctgtatctt anccgatttg cagagttgtt gaagaggatc acgaactact 780
 ccaaatttgt gtgtgaatac tgtcaatcan ctgaaagtca caanatcata caactgcaag 840
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 His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr
 35 40 45
 Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln
 50 55 60
 Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe
 65 70 75 80
 Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa

85

90

95

Glu	Lys	Lys	Phe	Pro	Lys	Thr	Ser	His	Val	Gly	Phe	Gly	Leu	Phe	Leu
			100				105						110		
Val	Gln	Asp	Gly	Lys	Arg	Phe	Arg	Thr	Arg	Ser	Thr	Glu	Val	Val	Arg
			115				120						125		
Leu	Val	Glu	Leu	Leu	Asp	Glu	Ala	Lys	Ser	Arg	Ser	Lys	Ser	Glu	Leu
			130				135						140		
Thr	Glu	Asn	Gly	Lys	Ile	Val	Asp	Trp	Thr	Asp	Xaa	Glu	Leu	Glu	Gln
145				150						155			160		
Thr	Ser	Glu	Ala	Val	Gly	Tyr	Gly	Ala	Val	Lys	Tyr	Ala	Asp	Leu	Lys
			165						170			175			
Asn	Asn	Arg	Leu	Thr	Asn	Tyr	Thr	Phe	Ser	Phe	Glu	Gln	Met	Leu	Ser
			180				185						190		
Asp	Lys	Gly	Asn	Thr	Ala	Val	Tyr	Leu	Gln	Tyr	Ala	His	Ala	Arg	Ile
			195				200						205		
Cys	Ser	Ile	Ile	Arg	Lys	Ser	Asn	Lys	Asn	Val	Xaa	Asp			
			210				215						220		

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ggttttggg attaccagt caacaatgct atgagtgtat tttcaagaat aagaggatcc 180
gcaacaaaact tccgtaaccc catggcagtt gggcaggcaa ttgcaaataa cctccccag 240
tcaaataatta tcgaatccat ctctgttgcc ggancgtggt acattaacat aacgttatcc 300
agcaattgga ttgcacagag gatacaaaga catgcttggt tgtgggaatc aaaacatggg 360
gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420
aaaaagaana tgcaagtgg gcaataatna agncaacaa taaatngggg natancccaa 480
ctcaaaangg ttgnggntca caaaanggtt aanttcntcn acgtaaacan gttgggaaac 540
nggggnacac a 551

<210> 26
<211> 68
<212> PRT
<213> Oryza sp.

<220>
<221> UNSURE
<222> (51)
<223> Xaa = ANY AMINO ACID

<400> 26
Phe Gly Asp Tyr Gln Cys Asn Asn Ala Met Ser Val Phe Ser Arg Ile
1 5 10 15
Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro Met Ala Val Gly Gln Ala
20 25 30
Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val
35 40 45
Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala
50 55 60
Gln Arg Ile Gln
65

<210> 27
<211> 411
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (18)
<223> n = A, C, G or T

<220>

<221> unsure
<222> (35)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (51)
<223> n = A, C, G or T

<220>
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<222> (159)
<223> n = A, C, G or T

<220>
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<222> (165)
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<220>
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<222> (286)
<223> n = A, C, G or T

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<222> (288)
<223> n = A, C, G or T

<220>
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<222> (325)
<223> n = A, C, G or T

<220>
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<222> (342)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (373)
<223> n = A, C, G or T

<400> 27
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acaactgata tagcatcact ttggtatcgt ctaaataagag aaaaacttga atggattgta 120
tatgttacag atattgggca gcaacagcac ttgatatnc tattnaaggc ctataggcgt 180
gcagggttggg taccaaagga tgagaatgag tatccaaaat gtactcatat aggttttggg 240
cttgttcttg gggaagatgg aaaacgattt cggactcgca ncagtnangt tggtcgatta 300
gttgattact tgatgaagct aaaangcgt gtaaaattgc cntcttgaaa cgtgatacaa 360
ctaaaggatt ggnctgaagg aggagatcga gaaaacatcc gaagcagttg g 411

<210> 28
<211> 115

<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (6)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (12)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (17)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (53)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (55)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (94)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (96)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (109)
<223> Xaa = ANY AMINO ACID

<400> 28
Val Glu Gly Val Asp Xaa Pro Leu Ile Ala Val Xaa Arg Asp Gly Gly
1 5 10 15
Xaa Asn Tyr Phe Thr Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn
20 25 30
Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln
35 40 45
Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu
50 55 60
Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
65 70 75 80
Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa

Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys
 100 105 110

Leu Pro Ser
 115

<210> 29
 <211> 565
 <212> DNA
 <213> Triticum sp.

<220>
 <221> unsure
 <222> (350)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (378)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (408)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (414)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (432)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (433)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (444)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (452)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (458)
 <223> n = A, C, G or T

<220>
 <221> unsure

<222> (466)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (487)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (494)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (503)
<223> n = A, C, G or T

<220>
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<222> (523)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (535)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (539)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (548)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (555)
<223> n = A, C, G or T

<400> 29
tgtttttcaa ggctgccagg atggctgggt ggcttccaga tccaaaggaa aagaagttcc 60
caaaaacgag tcatgttggg tttggccttg ttcttggagc agatggcaag cgcttccgaa 120
ctcgtagtac tgagggttgtt cggttgggaa gacctacttg atgaggctaa atctcgaagt 180
aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattggtga ctggactgat 240
gaaggaacta agagcaaact tcaaaaggca gtaagatatg gcgctgtcaa agtatgcggg 300
tctgaaagaa taaccgactg actaattaca cttcaacttt gattcaagan ctaagtgaca 360
agggaataac tgctgtcnac ttcaataagc caagcccgta cctccanca ttcnaaaacc 420
caacatggtg tnnaaaacta aaangatggg anattccncc tgccanccaa atagctgcct 480
gggacgnact aacngtatgc aanatgtaa aaggatgaca acncttccaa tgtcngggng 540
aaactatnac taccnaagta aaagt 565

<210> 30
<211> 33
<212> PRT
<213> Triticum sp.

<400> 30
 Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu
 1 5 10 15

Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
 20 25 30

Leu

<210> 31
 <211> 546
 <212> DNA
 <213> Oryza sp.

<220>
 <221> unsure
 <222> (448)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (512)
 <223> n = A, C, G or T

<400> 31
 atcactatatt cccctgatg tactcatcaa gagttttgag gatagatgga aggacacagg 60
 cattctccag gagtctgaaa gtggttttgc taaagaagcg gctgagcttt tgaaggatgg 120
 catcgatttg atcactgatg ctgacgcagc cctttcaaac ctgttgctcg atccccctcca 180
 tgctacatta agcagtgatg aagctaaatc tgtggtgcaa gacaagcttt ctgaggttgc 240
 atcaggactc atttctgctt atgatatcggt tgaactttgt caagcactag ctgagggccg 300
 tgatgggttg cagaagtggg tgaaaatttt tggcaaatca cttaaaagaa agggaaagtc 360
 actctttatg ccgctccgtg tactgctgac tggcaagctt catgggcctg acatgggcgg 420
 caccgtagtc ctcatacaca aagccggnac tgtggagcgg tcaactcaaca atccggtttc 480
 gtaaattctcg acgagagggtc agaatcctga angagtggag tggagtcact ggtacaggac 540
 aagatc 546

<210> 32
 <211> 147
 <212> PRT
 <213> Oryza sp.

<400> 32
 Pro Pro Asp Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr
 1 5 10 15

Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu
 20 25 30

Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu
 35 40 45

Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu
 50 55 60

Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu
 65 70 75 80

Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly
 85 90 95

Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys
100 105 110

Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly
115 120 125

Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys
130 135 140

Ala Gly Thr
145

<210> 33
<211> 524
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (386)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (423)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (459)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (481)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (483)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (486)
<223> n = A, C, G or T

<400> 33
aaatggcgct gttgtgtggc ggcatgccat ggtcgaaggt gatagttcct cccattttcc 60
accactctca caccctctgc accttcttct tccaacgacg ccgtttctca gtctctgctc 120
tctccgaaca accaccaccc gttcgcgttc gtttcgctcc ttctcccacc ggaaacctcc 180
acgtcggcgg tgcccgaacg gccctcttca actacttggt cgcaaggtcc aaaggtggga 240
aatttgtgct gagaattgag gacactgact tggagagggt caagtaggga gtctgaggag 300
gccatgctca aagatctttc ttggcttgga cttgattggg atgaagggcc tgggtgttgg 360
aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420
ggngaaacta cacaaatccg ggcaagtta accgctgcnt tctgggtccaa agaggggaact 480
nanagnaaat gaaaggaggt tgctaaacta aagcaactgg cccc 524

<210> 34

<211> 94
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (63)
<223> Xaa = ANY AMINO ACID

<400> 34
Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro
1 5 10 15
Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly
20 25 30
Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
35 40 45
Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser
50 55 60
Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
65 70 75 80
Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro
85 90

<210> 35
<211> 506
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (18)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (483)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (505)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (506)
<223> n = A, C, G or T

<400> 35
ggaacatgga tattattngt gttcccgggg ttatggctga agcagagctt atagcttcta 60
tcgtcacttt gtttaagcga ataggaatta cagaatcaga tgtcggattt aaggtttcca 120
gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180
aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240
tgaaagctgt tggctctatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300
agtcattgac cgagttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360

acagtattct cccttgctga aaaaattggt tactctaaat ggttcaattt gatgatagtt 420
gttcgaggtc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480
gcntctgtgt gtgtcaatac attgnn 506

<210> 36
<211> 48
<212> PRT
<213> Glycine max

<400> 36
Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
1 5 10 15
Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
20 25 30
Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
35 40 45

<210> 37
<211> 577
<212> DNA
<213> Triticum sp.

<220>
<221> unsure
<222> (140)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (370)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (411)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (413)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (469)
<223> n = A, C, G or T

<220>
<221> unsure
<222> (481)
<223> n = A, C, G or T

<220>
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<222> (504)
<223> n = A, C, G or T

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<221> unsure
 <222> (575)
 <223> n = A, C, G or T

<220>
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 <222> (530)
 <223> n = A, C, G or T

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 <222> (551)
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 <222> (556)
 <223> n = A, C, G or T

<220>
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 <222> (564)
 <223> n = A, C, G or T

<400> 37
 cttgggatta catcttctga tgtgggggatc agactgtcca gccgaaaggt tctacaggcc 60
 gtgtttggata tgtactccgt accacaacac ttgtttactc aagtttgtgt tattgttgac 120
 aagctgggga aactgagtan ggaagaaatt gagaaggaat tgatttcaac tgggctgtca 180
 tctgaagcag tacagggcat cattgaagtg ctctctctca agtcactgtc caaacttgaa 240
 gaggtgctag gctcaggtgt tgaagccgtt gctgacttga agaacctctt ctgcttgct 300
 gagcaatatg gttattctga ttggatctgt ttgatgcat ctgttggtcg tggccttgca 360
 tactacacan gggattgttt ttgaggcttt tgatagggaa gggaaactga nancatttgt 420
 ggtggggggg aggtatgaca ggctacgtca acatttggaa ctgaagatnt ccaccctgtg 480
 nctttggatt tggaatcctg tcanagtga ctcnaaaga aaggtcttn ctacctgcac 540
 tcaaataata nattgntcca ttgncaagac ttggggg 577

<210> 38
 <211> 46
 <212> PRT
 <213> Triticum sp.

<220>
 <221> UNSURE
 <222> (38)
 <223> Xaa = ANY AMINO ACID

<400> 38
 Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr
 1 5 10 15
 Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys
 20 25 30
 Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile
 35 40 45